

104769 1000000000

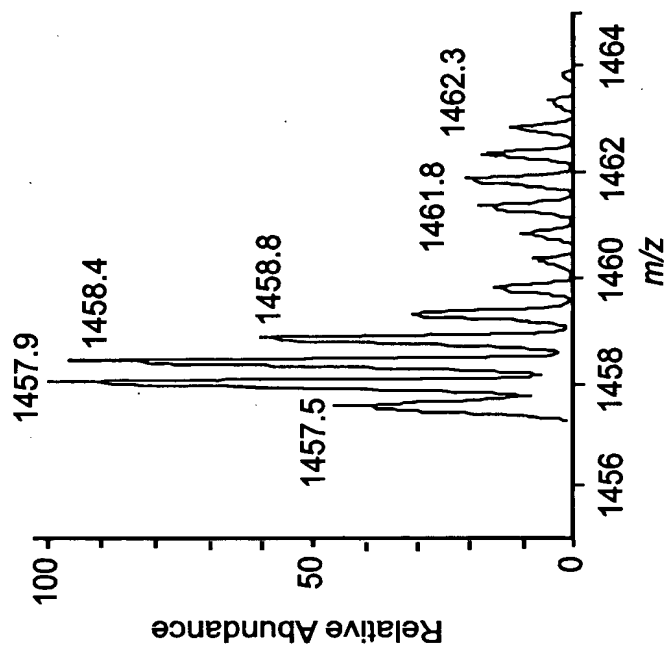


FIG. 1A

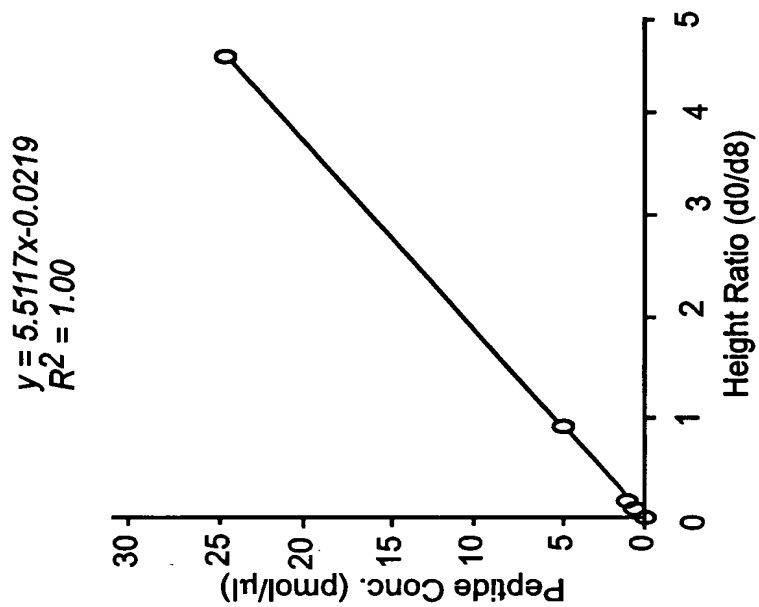


FIG. 1B

Mass spectrum of the peptide L-D-Q-W-L-C-E-K (monoisotopic mass: 1522.7) showing relative abundance versus  $m/z$ . The spectrum displays several peaks corresponding to the peptide and its fragments. Key features include:

- Peptide Ion:** The base peak is at  $m/z$  1522.7, labeled as  $[M+2H]^{2+}$ .
- Biotin Cleavage Sites:** Indicated by arrows pointing to peaks at  $m/z$  283.2 (labeled "Biotin cleavage") and 283.2 (labeled "C+biotin").
- Other Labeled Peaks:**
  - $m/z$  1237.7 (labeled "Q")
  - $m/z$  1237.7 (labeled "D")
  - $m/z$  1000.0 (labeled "L")
  - $m/z$  1000.0 (labeled "W")
  - $m/z$  800.0 (labeled "K")
  - $m/z$  575.0 (labeled "E")
  - $m/z$  575.0 (labeled "O")
  - $m/z$  575.0 (labeled "W")
  - $m/z$  575.0 (labeled "L")

4. 7. 88

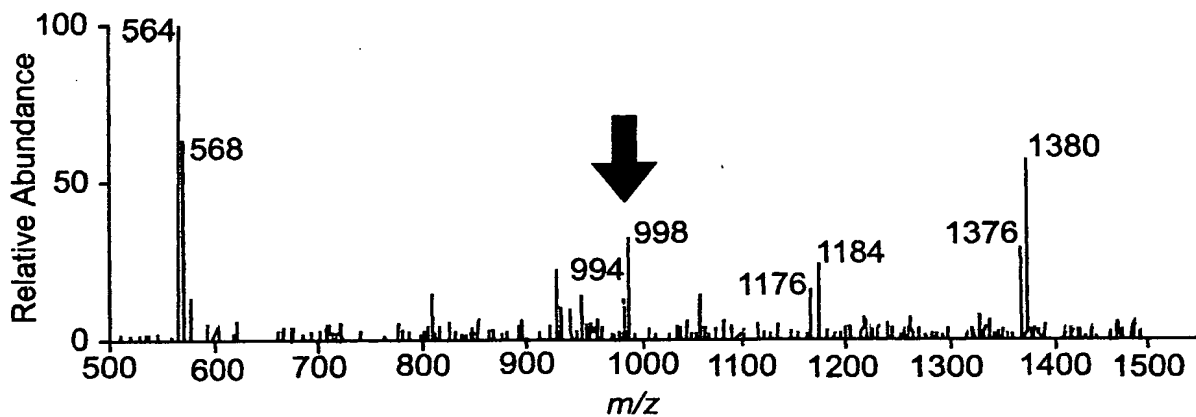


FIG. 3A

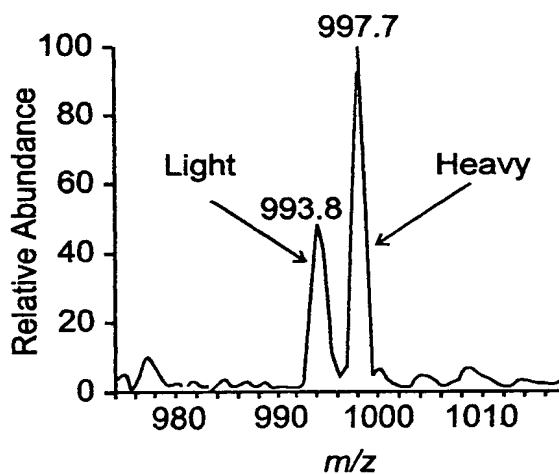


FIG. 3B

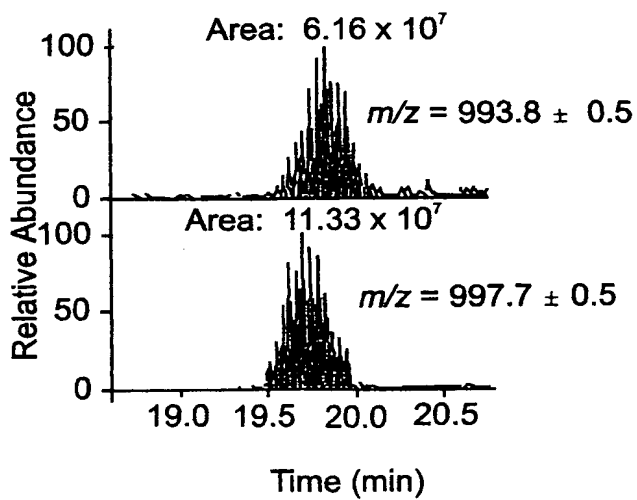


FIG. 3C

FOI 60 1000000

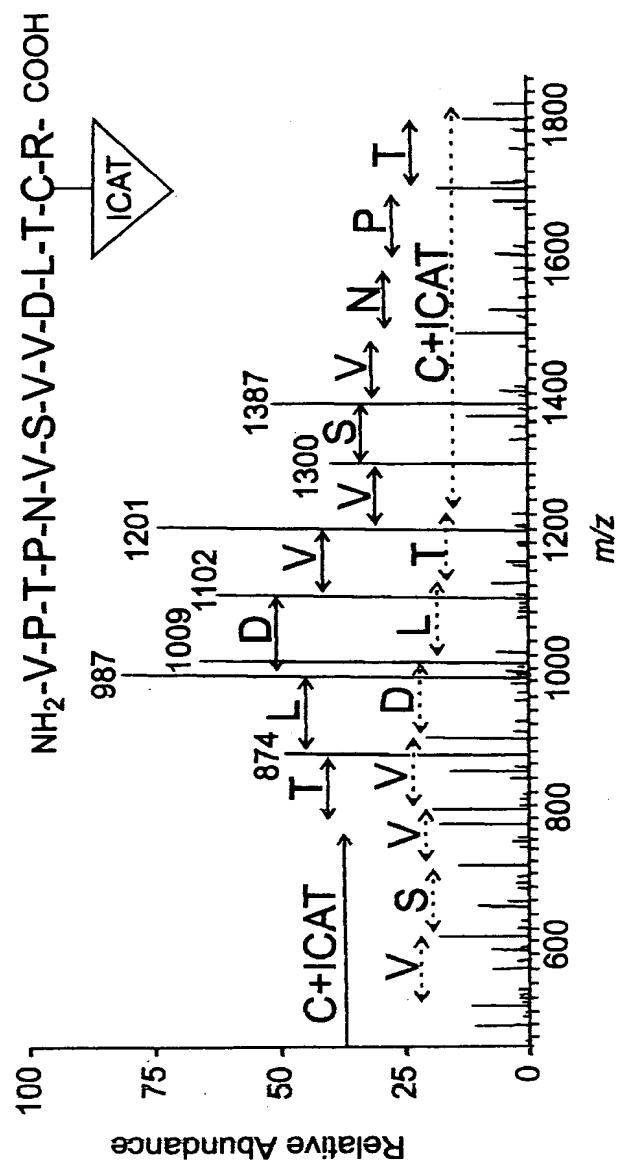


FIG. 4A

#	Rank/Sp	$(M+H)^+ \times 10^{-4}$	Ions	Reference	Peptide
1.	1/ 1	1994.3 4.4675	17/26	G3P_RABIT	(R)VPTPNVSVVDLTC#R (SEQ ID NO:60)
2.	2/403	1995.1 2.7366	13/34	SLTRNGL	(E)LGKPPVLTANQVTIWEGLR (SEQ ID NO:61)
3.	3/ 3	1995.0 2.6591	16/36	FLP_LACCA	(N)LANPNVYTETLTAATVCTI (SEQ ID NO:62)
4.	4/209	1995.0 2.6335	14/36	A42912	(Y)LALLPSDAEGPHGQFVTDK (SEQ ID NO:63)
5.	5/381	1995.1 2.4634	13/38	H69373	(L)ALLVLVAPAMAAANGEDLRN (SEQ ID NO:64)

FIG. 4B

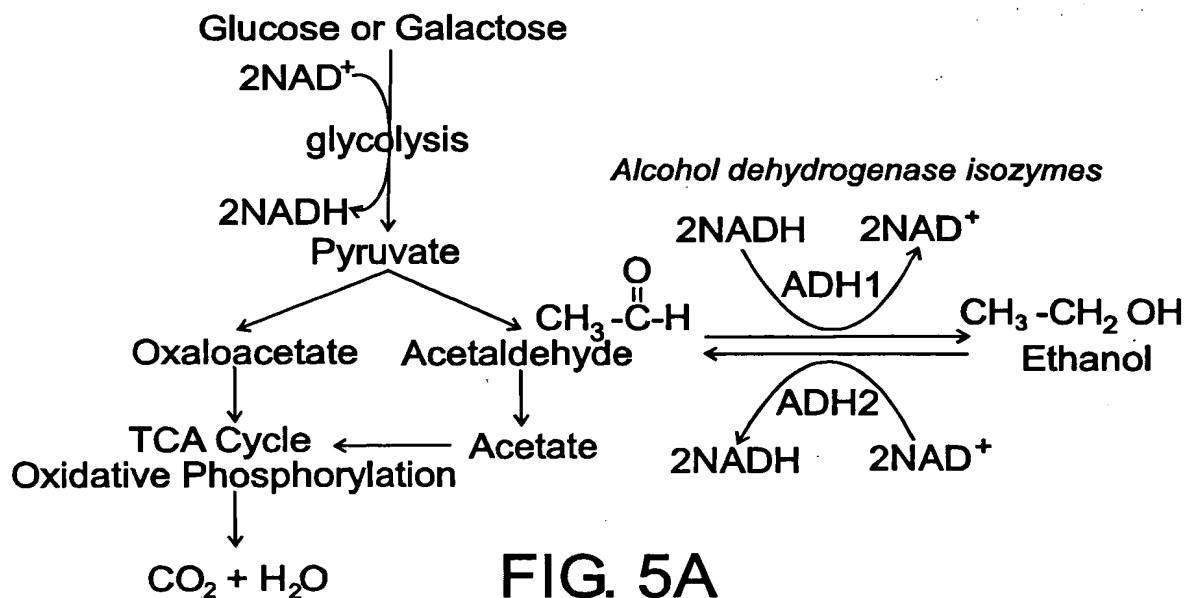
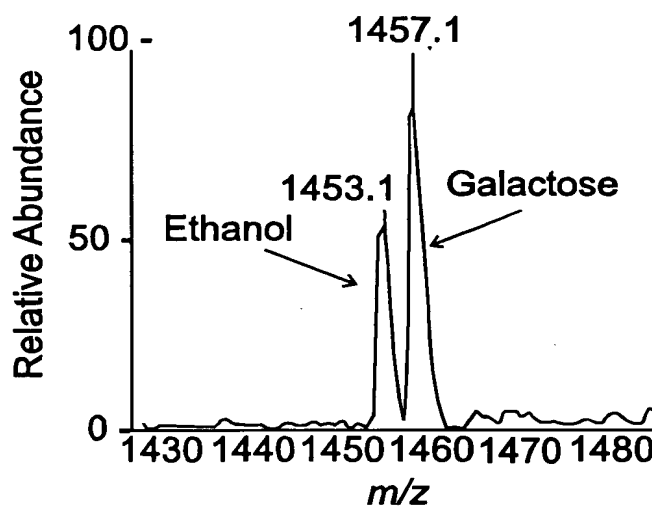


FIG. 5A

ADH1 : YSVC#HTDLHAWHGDWPLPVK

FIG. 5B



ADH2 : YSVC#HTDLHAWHGDWPLPIK

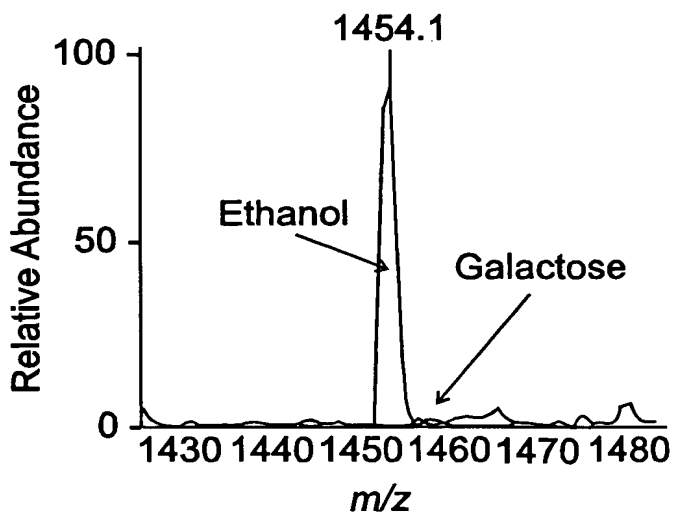


FIG. 5C

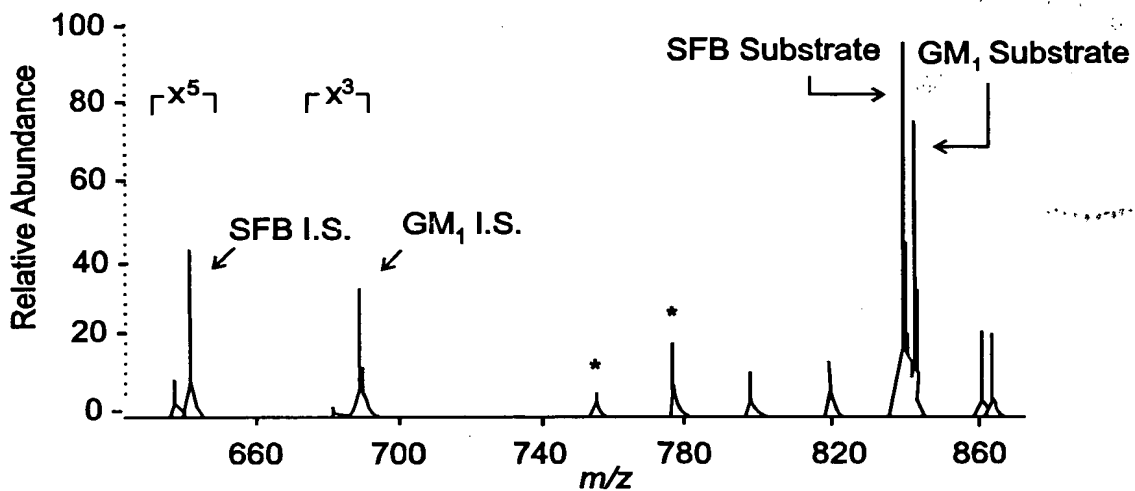


FIG. 6A

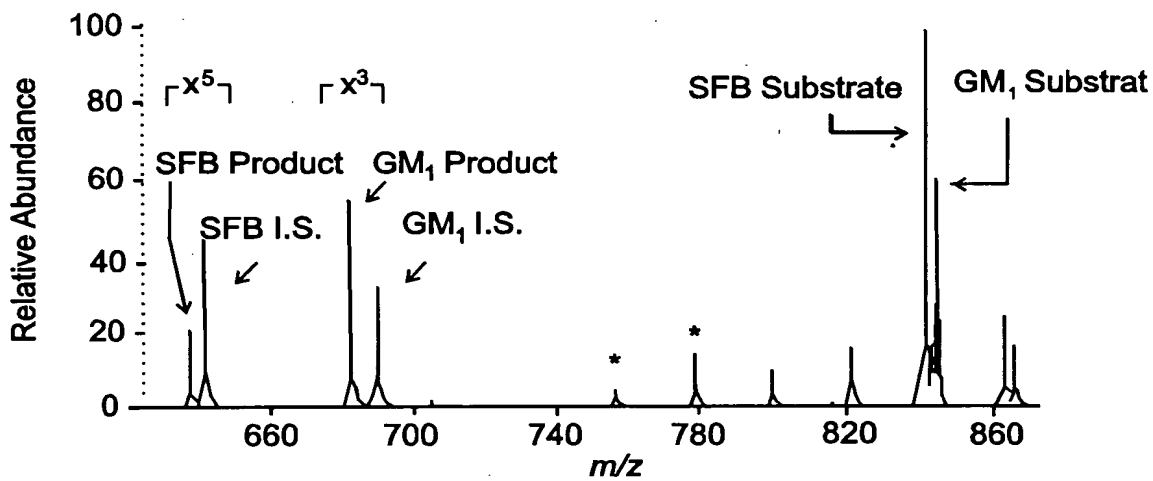


FIG. 6B

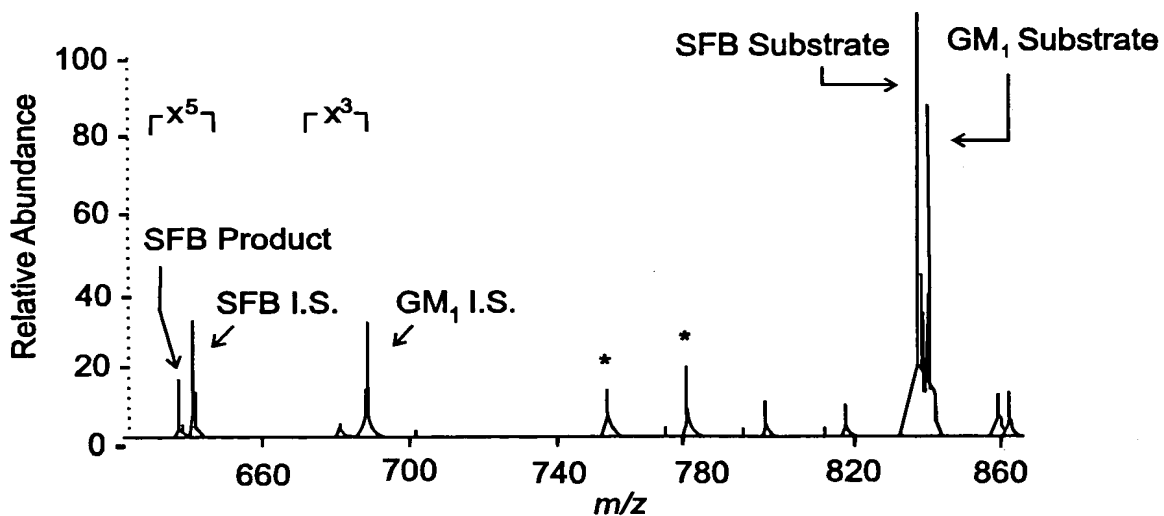


FIG. 6C

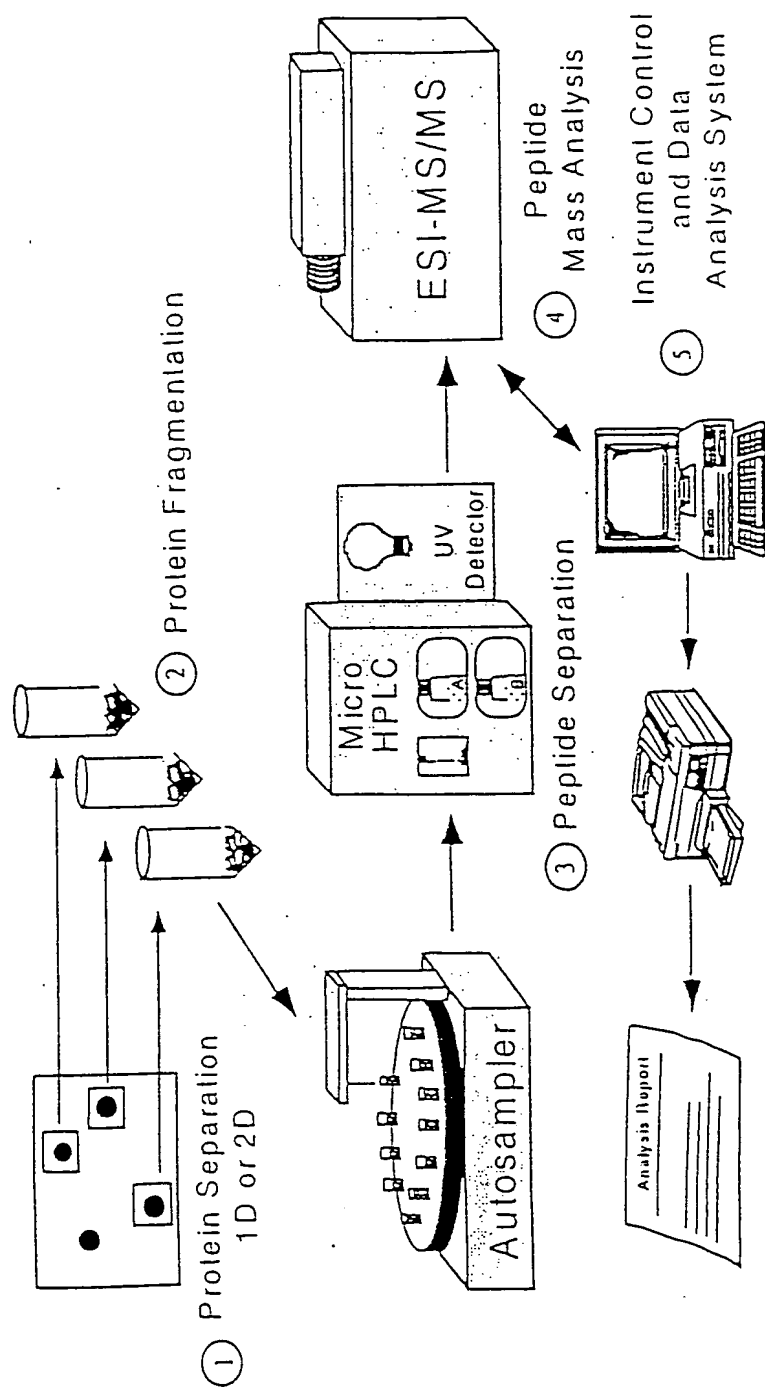


FIG. 7

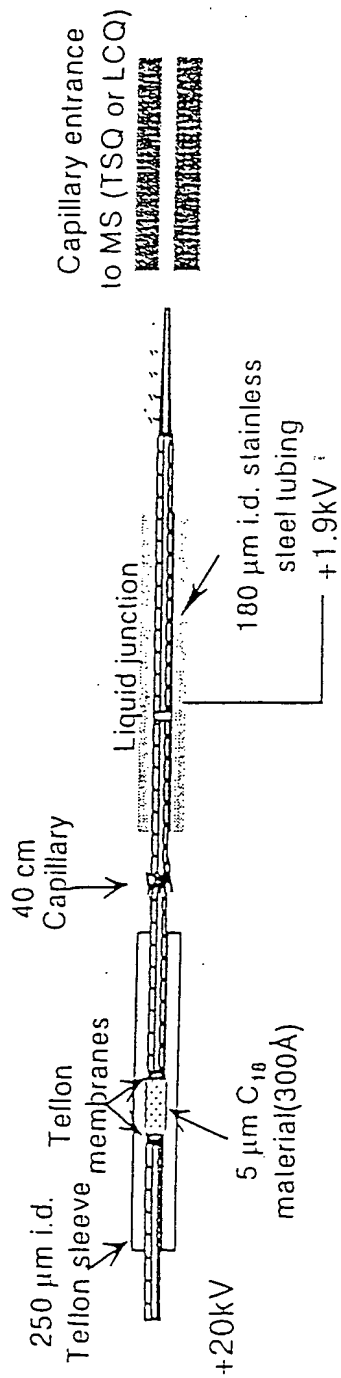


FIG. 8A

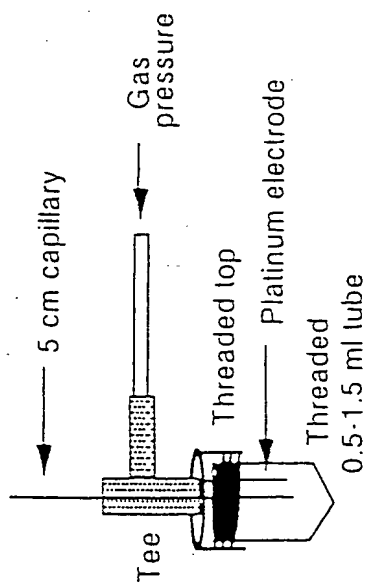


FIG. 8B